



0500 #4

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/670,756

Source: OIP

Date Processed by STIC: 10/4/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version of the rules effective October 1, 1997 (new rules). The World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is 1.2K compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/670,756

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 _____ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 _____ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 _____ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 _____ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 _____ Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 _____ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 _____ Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES" response to include the skipped sequence(s).
- 9 _____ Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence
<210> sequence id number
<400> sequence id number
000
- 10 _____ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 _____ Use of <213> Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown".
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 12 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file resulting in missing or misaligned by product identifiers and responses (as indicated in raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

P. 6

1415 11/01/2014

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1 1100 APPLICANT: BLANCO, JOSEPH
2 1101 BETTEL, MARIA
3 1102 LINA, BRUNO-PEDRO
4 1103 AN, WENJIAN
5 1104 TITLE OF INVENTION: 1-DIMENSION CHANNEL INTERACTIONS AND USE THEREOF
6 1105 FILE REFERENCE: NIN-00-0071
7 1106 CURRENT APPLICATION NUMBER: US/09/670,756
8 1107 CURRENT FILING DATE: 2000-09-27
9 1108 PRIOR APPLICATION NUMBER: USN 08/110,633
10 1109 PRIOR FILING DATE: 1998-11-25
11 1110 PRIOR APPLICATION NUMBER: USN 08/210,533
12 1111 PRIOR FILING DATE: 1998-11-25
13 1112 PRIOR APPLICATION NUMBER: USN 08/210,533
14 1113 PRIOR FILING DATE: 1999-04-29
15 1114 PRIOR APPLICATION NUMBER: USN 08/150,814
16 1115 PRIOR FILING DATE: 1998-03-07
17 1116 PRIOR APPLICATION NUMBER: USN 08/250,001
18 1117 PRIOR FILING DATE: 1998-03-09
19 1118 PRIOR APPLICATION NUMBER: USN 08/180,192
20 1119 PRIOR FILING DATE: 1998-03-21
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24 1123 PRIOR FILING DATE: 1999-11-19
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RAW SEQUENCE LISTING

2014 年 12 月 1 日

PAPER: APPLICATION US/09/670,756

Figure 1. A schematic diagram of the experimental design.

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RAW SEQUENCE LISTING

PATENT APPLICATION US/09/670,756

DATE: 12/12/2009

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125 31 45
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127 46 60
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129 61 75
130 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Thr Leu Phe Asn
131 76 90
132 Ala Phe Asp Thr Thr Gln Thr Glu Ser Val Lys Phe Glu Asp Phe Val
133 91 105
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135 106 120
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137 121 135
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139 136 150
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141 151 165
142 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
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160 ggggaataa gaggaaagat taactgaat taagaattt cctatgaatt ggaatatac
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RAW SEQUENCE LISTING

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PAID: ALLIANCE N US/09/670,756

2000

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 221 Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
 222 45 10 15
 223 Asp Asp Lys Ile Gln Asp Asp Leu Leu Met Thr Met Val Cys His Arg
 224 50 55 60
 225 Pro Gln Gly Leu Gln Gln Leu Gln Ala Gln Thr Asn Phe Thr Lys Arg
 226 65 70 75 80
 227 Gln Leu Gln Val Leu Tyr Arg Gly Phe Leu Arg Gln Cys Pro Ser Gly
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 229 Val Val Asn Gln Gln Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro
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 231 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Arg Ala Phe Asp
 232 115 120 125
 233 Thr Thr Gln Thr Gly Ser Val Lys Phe Gln Asp Phe Val Thr Ala Leu
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 235 Ser Ile Leu Leu Thr Gly Thr Val His Gln Leu Leu Arg Thr Phe
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 237 Arg Leu Thr Asp Ile Val Lys Arg Tyr Thr Ile Asn Arg Gln Thr Met
 238 165 170 175 180
 239 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Thr
 240 185 190 195 200
 241 His Val Leu Lys Gln Asp Thr Pro Arg Tyr His Val Asp Val Phe Phe
 242 205 210 215
 243 Gln Lys Met Asp Lys Arg Lys Asp Gly Ile Val Thr Leu Asp Gln Phe
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 245 Leu Gln Ser Cys Gln Gln Asp Asp Asn Ile Met Arg Ser Leu Gln Leu
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Asp Leu Ser Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val
 35 40 45

Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
 50 55 60

Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 65 70 75 80

Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Xaa Ile Tyr Ala Gln
 85 90 95

Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 100 105 110

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 115 120 125

Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
 130 135 140

Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 145 150 155 160

Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
 165 170 175

Tyr Thr Tyr Leu Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Asp
 180 185 190

Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp
 195 200

See item 10
 on Error
 Summary
 sheet

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

US/09/670,756

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), and 10⁹ cells/ml (d). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), and 10⁹ cells/ml (d). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), and 10⁹ cells/ml (d).

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